



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,588A
 Source: 1600 RUSH
 Date Processed by STIC: 9/26/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

#9

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/701,588A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

#9



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/701,588A

DATE: 09/26/2002
TIME: 10:49:12

Input Set : A:\PTO.txt
Output Set: N:\CRF4\09262002\I701588A.raw

ppr 1-7

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: UNITED BIOMEDICAL INC., ET AL.
- 7 (ii) TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
- 8 EPITOPE AS IMMUNE STIMULATORS FOR SYNTHETIC
- 9 PEPTIDE IMMUNOGENS
- 11 (iii) NUMBER OF SEQUENCES: 151
- 13 (iv) CORRESPONDENCE ADDRESS:
 - 14 (A) ADDRESSEE: Morgan & Finnegan, L.L.P.
 - 15 (B) STREET: 345 Park Avenue
 - 16 (C) CITY: New York
 - 17 (D) STATE: NY
 - 18 (E) COUNTRY: USA
 - 19 (F) ZIP: 10154-0054
- 21 (v) COMPUTER READABLE FORM:
 - 22 (A) MEDIUM TYPE: Floppy disk
 - 23 (B) COMPUTER: IBM PC compatible
 - 24 (C) OPERATING SYSTEM: PC Windows
 - 25 (D) SOFTWARE: Word 97
- 27 (vi) CURRENT APPLICATION DATA:
 - 28 (A) APPLICATION NUMBER: US/09/701,588A
 - 29 (B) FILING DATE: 21-Jun-1999
 - 30 (C) CLASSIFICATION:
- 32 (vii) PRIOR APPLICATION DATA:
 - 33 (A) APPLICATION NUMBER: 09/100,414
 - 34 (B) FILING DATE: 20-JUNE-1998
- 36 (viii) ATTORNEY/AGENT INFORMATION:
 - 37 (A) NAME: Maria H. Lin
 - 38 (B) REGISTRATION NUMBER: 29,323
 - 39 (C) REFERENCE/DOCKET NUMBER: 1151-4158PC1
- 41 (ix) TELECOMMUNICATION INFORMATION:
 - 42 (A) TELEPHONE: 212-758-4800
 - 43 (B) TELEFAX: 212-751-6849

ERRORED SEQUENCES

- 93 (2) INFORMATION FOR SEQ ID NO: 4:
- 94 (i) SEQUENCE CHARACTERISTICS:
 - 95 (A) LENGTH: 16 amino acids
 - 96 (B) TYPE: amino acid
 - 97 (D) TOPOLOGY: LINEAR
- 99 (ii) MOLECULE TYPE: peptide

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
103 Asp Val Ser Asp Val Lys Gly Val Val Val His Lys
104 1 5 10
105 Val Asp Gly Val 15-15 misaligned amino acid nos. - see item 3
E--> 106 on Error summary sheet

124 (2) INFORMATION FOR SEQ ID NO: 6:
126 (i) SEQUENCE CHARACTERISTICS:
127 (A) LENGTH: 15 amino acids
128 (B) TYPE: amino acid
129 (D) TOPOLOGY: linear
131 (ii) MOLECULE TYPE: peptide
133 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
135 Ile Ser Glu Ile Lys Gly Val Ile Val His Lys Ile
136 1 5 10 same error
137 Glu Gly Ile 15
138
156 (2) INFORMATION FOR SEQ ID NO: 8:
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 15 amino acids
160 (B) TYPE: amino acid
161 (D) TOPOLOGY: linear
163 (ii) MOLECULE TYPE: peptide
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
167 Leu Ser Glu Ile Lys Gly Val Ile Val His Lys
E--> 168 1 5 10 same
169 Leu Glu Gly Val 15-15
E--> 170
789 (2) INFORMATION FOR SEQ ID NO: 46:
791 (i) SEQUENCE CHARACTERISTICS:
792 (A) LENGTH: 45 amino acids
793 (B) TYPE: amino acid
794 (D) TOPOLOGY: linear
797 (ii) MOLECULE TYPE: peptide
799 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
801 Thr Ala Lys Ser Lys Lys Phe Pro Ser Tyr Thr Ala
802 1 5 10
803 Thr Tyr Gln Phe Gly Gly Ile Thr Glu Ile Arg Thr
804 15 20
805 Val Ile Val Thr Arg Ile Glu Thr Ile Gly Gly Glu
806 25 30 35
807 His Trp Ser Tyr Gly Leu Arg Pro Gly
E--> 808 40 45<insert
1209 (2) INFORMATION FOR SEQ ID NO: 68
1211 (i) SEQUENCE CHARACTERISTICS:
1212 (A) LENGTH: 30 amino acids
1213 (B) TYPE: amino acid
1214 (D) TOPOLOGY: linear
1216 (ii) MOLECULE TYPE: peptide
1218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68 3

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Input Set : A:\PTO.txt
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1220 Lys Lys Lys Val Arg Val Val Thr Lys Val Val Thr
1221 1 5 10
1222 Val Pro Ile Ser Val Asp Gly Gly Glu His Trp Ser
1223 15 20
1224 Tyr Gly Leu Arg Pro Gly
E--> 1225 25 30 *L*
1681 (2) INFORMATION FOR SEQ ID NO: 94:
1683 (i) SEQUENCE CHARACTERISTICS:
1684 (A) LENGTH: 46 amino acids
1685 (B) TYPE: amino acid
1686 (D) TOPOLOGY: linear
1688 (ii) MOLECULE TYPE: peptide
1691 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:
1693 Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
1694 1 5 10
1695 Arg Ile Glu Thr Ile Leu Phe Gly Gly Cys Gly Glu
1696 15 20
1697 Thr Tyr Gln Ser Arg Val Thr His Pro His Leu Pro
E--> 1698 25 30 35 35
1699 Arg Ala Leu Met Arg Ser Thr Thr Lys Cys
E--> 1700 40 40 45 45
1743 (2) INFORMATION FOR SEQ ID NO: 97:
1745 (i) SEQUENCE CHARACTERISTICS:
1746 (A) LENGTH: 42 amino acids
1747 (B) TYPE: amino acid
1748 (D) TOPOLOGY: linear
1750 (ii) MOLECULE TYPE: peptide
1752 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:
1754 Leu Ser Glu Ile Lys Gly Val Ile Val His Lys Leu
1755 1 5 10
1756 Glu Gly Val Gly Gly Cys Gly Glu Thr Tyr Gln Ser
1757 15 20
1758 Arg Val Thr His Pro His Leu Pro Arg Ala Leu Met
E--> 1759 25 30 35 35
1760 Arg Ser Thr Thr Lys Cys
E--> 1761 40 40
2297 (2) INFORMATION FOR SEQ ID NO: 126:
2299 (i) SEQUENCE CHARACTERISTICS:
2300 (A) LENGTH: 51 amino acids
2301 (B) TYPE: amino acid
2302 (D) TOPOLOGY: linear
2304 (ii) MOLECULE TYPE: peptide
2306 (ix) FEATURE:
2307 (A) NAME/KEY: Modified site
2308 (B) LOCATION 22?
L--> 2309 (D) OTHER INFORMATION: /note= "(e-N)Lys" ?
2311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:
2313 Ile Ser Ile Ser Glu Ile Lys Gly Val Ile Val His
2314 1 5 10

PL

Ser is at location 22

do you mean
location 20?
(Xaa)

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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(W) 2315 Lys Ile Glu Gly Ile Leu Phe Xaa Glu Ser Val Glu
 2316 15 20
 2317 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2318 25 30 35
 2319 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
 E--> 2320 40 48
 2321 Thr Gly Asp 45
 2322 50

2324 (2) INFORMATION FOR SEQ ID NO: 127:

2326 (i) SEQUENCE CHARACTERISTICS:
 2327 (A) LENGTH: 51 amino acids
 2328 (B) TYPE: amino acid
 2329 (D) TOPOLOGY: linear
 2331 (ii) MOLECULE TYPE: peptide
 2334 (ix) FEATURE:

(A) NAME/KEY: Modified site
 (B) LOCATION: 22

C--> 2337 (D) OTHER INFORMATION: /note= "(e-N)Lys"
 2339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:
 2341 Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
 2342 1 5 10
 W--> 2343 Arg Ile Glu Thr Ile Leu Phe Xaa Glu Ser Val Glu
 2344 15 20
 2345 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2346 25 30 35
 2347 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala

E--> 2348 40 48
 2349 Thr Gly Asp 45
 2350 50

2352 (2) INFORMATION FOR SEQ ID NO: 128:

2354 (i) SEQUENCE CHARACTERISTICS:
 2355 (A) LENGTH: 51 amino acids
 2356 (B) TYPE: amino acid
 2357 (D) TOPOLOGY: linear
 2359 (ii) MOLECULE TYPE: peptide
 2361 (ix) FEATURE:

(A) NAME/KEY: Modified site
 (B) LOCATION: 20

(Q) 2364 (D) OTHER INFORMATION: /note= "(e-N)Lys"
 2366 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:
 2368 Ile Ser Leu Thr Glu Ile Arg Thr Val Ile Val Thr
 2369 1 5 10

(W) 2370 Arg Leu Glu Thr Val Leu Phe Xaa Glu Ser Val Glu
 2371 15 20
 2372 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2373 25 30 35
 2374 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
 E--> 2375 40 48
 2376 Thr Gly Asp 45

*do you mean location
20?*

RAW SEQUENCE LISTING
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Input Set : A:\PTO.txt
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2377 50
 2379 (2) INFORMATION FOR SEQ ID NO: 129:
 2381 (i) SEQUENCE CHARACTERISTICS:
 2382 (A) LENGTH: 51 amino acids
 2383 (B) TYPE: amino acid
 2384 (D) TOPOLOGY: linear
 2386 (ii) MOLECULE TYPE: peptide
 2388 (ix) FEATURE:
 2389 (A) NAME/KEY: Modified site
 2390 (B) LOCATION: 20
 C--> 2391 (D) OTHER INFORMATION: /note= "(e-N)Lys"
 2393 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:
 2395 Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
 2396 1 5 10
 Q--> 2397 Arg Ile Glu Thr Val Ile Phe Xaa Glu Ser Val Glu
 2398 15 20
 2399 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2400 25 30 35
 2401 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
 E--> 2402 40 48
 2403 Thr Gly Asp 45
 2404 50
 2772 (2) INFORMATION FOR SEQ ID NO: 148:
 2774 (i) SEQUENCE CHARACTERISTICS:
 2775 (A) LENGTH: 52 amino acids
 2776 (B) TYPE: amino acid
 2777 (D) TOPOLOGY: linear
 2779 (ii) MOLECULE TYPE: peptide
 2782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:
 2784 Ile Ser Ile Ser Glu Ile Lys Gly Val Ile Val His
 2785 1 5 10
 2786 Lys Ile Glu Gly Ile Leu Phe Gly Gly Glu Ser Val
 2787 15 20
 2788 Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
 E--> 2789 25 30 3635
 2790 Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr
 2791 40 45
 2792 Ala Thr Gly Asp
 2793 50
 2795 (2) INFORMATION FOR SEQ ID NO: 149:
 2797 (i) SEQUENCE CHARACTERISTICS:
 2798 (A) LENGTH: 52 amino acids
 2799 (B) TYPE: amino acid
 2800 (D) TOPOLOGY: linear
 2802 (ii) MOLECULE TYPE: peptide
 2804 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:
 2806 Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
 2807 1 5 10
 2808 Arg Ile Glu Thr Ile Leu Phe Gly Gly Glu Ser Val

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Input Set : A:\PTO.txt
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2809 15 20
 2810 Glu Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg
 E--> 2811 25 30 3635
 2812 Lys Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr
 2813 40 45
 2814 Ala Thr Gly Asp
 2815 50
 2817 (2) INFORMATION FOR SEQ ID NO: 150:
 2819 (i) SEQUENCE CHARACTERISTICS:
 2820 (A) LENGTH: 50 amino acids
 2821 (B) TYPE: amino acid
 2822 (D) TOPOLOGY: linear
 2824 (ii) MOLECULE TYPE: peptide
 2827 (ix) FEATURE:
 2828 (A) NAME/KEY: Modified site
 2829 (B) LOCATION: 20
 C--> 2830 (D) OTHER INFORMATION: /note= "(e-N)Lys"
 2832 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:
 2834 Ile Ser Leu Thr Glu Ile Arg Thr Val Ile Val Thr
 2835 1 5 10
 2836 Arg Leu Glu Thr Val Leu Phe Xaa Glu Ser Val Glu
 2837 15 20
 2838 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2839 25 30 35
 2840 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
 E--> 2841 40 48
 2842 Thr Gly 45
 2843 50
 2845 (2) INFORMATION FOR SEQ ID NO: 151:
 2847 (i) SEQUENCE CHARACTERISTICS:
 2848 (A) LENGTH: 50 amino acids
 2849 (B) TYPE: amino acid
 2850 (D) TOPOLOGY: linear
 2852 (ii) MOLECULE TYPE: peptide
 2854 (ix) FEATURE:
 2855 (A) NAME/KEY: Modified site
 2856 (B) LOCATION: 20
 C--> 2857 (D) OTHER INFORMATION: /note= "(e-N)Lys"
 2859 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:
 2861 Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
 2862 1 5 10
 2863 Arg Ile Glu Thr Val Ile Phe Xaa Glu Ser Val Glu
 2864 15 20
 2865 Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
 2866 25 30 35
 2867 Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
 E--> 2868 40 48
 2869 Thr Gly 45
 2870 50

See next page for more errors

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Ser Ile Thr Glu Ile Arg Thr Val Ile Val Thr
1 5 10
Arg Ile Glu Thr Val Ile Phe Xaa Glu Ser Val Glu
15 20
Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys
25 30 35
Ser Ile Arg Ile Gly Pro Gly Gln Ala Phe Tyr Ala
40 45
Thr Gly
50

CLAIMS

We claim:

1. A T helper cell epitope selected from the group consisting of SEQ ID NOS: 6-22, 105, 123, 124, 31-35.

sample of extraneous text at end of Sequence Listing. Please delete all of it. Do not insert claim information or any information other than the Sequence Listing.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/701,588A

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Input Set : A:\PTO.txt
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:82 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:97 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:106 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:113 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:136 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:168 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:808 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
L:1225 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:68
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
L:1698 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:94
M:332 Repeated in SeqNo=94
L:1759 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:97
M:332 Repeated in SeqNo=97
L:2204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120 after pos.:12
L:2222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:121 after pos.:12
L:2240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122 after pos.:12
L:2309 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:126 after pos.:12
L:2320 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:126
L:2337 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:12
L:2348 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:127
L:2364 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:12
L:2375 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:128
L:2391 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:129 after pos.:12
L:2402 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:129
L:2506 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136 after pos.:0
L:2530 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:0
L:2553 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:138 after pos.:0
L:2576 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:2599 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:2622 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:2645 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:2668 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143 after pos.:0
L:2691 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/701,588A

DATE: 09/26/2002
TIME: 10:49:14

Input Set : A:\PTO.txt
Output Set: N:\CRF4\09262002\I701588A.raw

L:2695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:0
L:2714 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145 after pos.:0
L:2737 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:0
L:2760 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147 after pos.:0
L:2789 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:148
L:2811 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:149
L:2830 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:150 after pos.:12
L:2841 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:150
L:2857 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:2863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151 after pos.:12
L:2868 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:151